

1

<110> SAKANO, SEIJI
ITO, AKIRA

<120> DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE

<130> KP-8447

<140> 09/068,740

<141> 1998-06-18

<150> JP 7-299611

<151> 1995-11-17

<150> JP 7-311811

<151> 1995-11-30

<150> PCT/JP96/03356

<151> 1996-11-15

<160> 48

<170> PatentIn Ver. 2.1

<210> 1

<211> 43

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (2) . . (4)

<223> Xaa is unknown

<220>

<221> UNSURE

<222> (7) . . (9)

<223> Xaa is unknown

<220>

<221> UNSURE

<222> (11) .. (13)

<223> Xaa is unknown

<220>

<221> UNSURE

<222> (20)

<223> Xaa is unknown

<220>

<221> UNSURE

<222> (24) .. (25)

<223> Xaa is unknown

<220>

<221> UNSURE

<222> (27) .. (29)

<223> Xaa is unknown

<220>

<221> UNSURE

<222> (31)..(33)

<223> Xaa is unknown

<220>

<221> UNSURE

<222> (35)..(36)

<223> Xaa is unknown

<220>

<221> UNSURE

<222> (39)

<223> Xaa is unknown

<220>

<221> UNSURE

<222> (41)..(42)

<223> Xaa is unknown

<400> 1

Cys Xaa Xaa Xaa Tyr Tyr Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Arg Pro
1 5 10 15

Arg Asx Asp Xaa Phe Gly His Xaa Xaa Cys Xaa Xaa Xaa Gly Xaa Xaa
20 25 30

Xaa Cys Xaa Xaa Gly Trp Xaa Gly Xaa Xaa Cys
35 40

<210> 2

<211> 200

<212> PRT

<213> Homo sapiens

<400> 2

Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe Val Asn Lys Lys Gly
1 5 10 15

Leu Leu Gly Asn Arg Asn Cys Cys Arg Gly Gly Ala Gly Pro Pro Pro
20 25 30

Cys Ala Cys Arg Thr Phe Phe Arg Val Cys Leu Lys His Tyr Gln Ala
35 40 45

Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly Ser Ala Val Thr Pro
50 55 60

Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp Gly Gly Gly Ala Asp
65 70 75 80

Ser Ala Phe Ser Asn Pro Ile Arg Phe Pro Phe Gly Phe Thr Trp Pro
85 90 95

TOGETHER

Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His Thr Asp Ser Pro Asp
 100 105 110

Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Ala Thr
 115 120 125

Gln Arg His Leu Thr Val Gly Glu Glu Thr Ser Gln Asp Leu His Ser
 130 135 140

Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr Arg Phe Val Cys Asp Glu
 145 150 155 160

His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys Arg Pro Arg Asp Asp
 165 170 175

Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly Glu Lys Val Cys Asn
 180 185 190

Pro Gly Trp Lys Gly Pro Tyr Cys
 195 200

<210> 3

<211> 520

<212> PRT

<213> Homo sapiens

<400> 3

Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe Val Asn Lys Lys Gly
 1 5 10 15

Leu Leu Gly Asn Arg Asn Cys Cys Arg Gly Gly Ala Gly Pro Pro Pro
 20 25 30

Cys Ala Cys Arg Thr Phe Phe Arg Val Cys Leu Lys His Tyr Gln Ala
 35 40 45

Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly Ser Ala Val Thr Pro
 50 55 60

Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp Gly Gly Gly Ala Asp
 65 70 75 80

Ser Ala Phe Ser Asn Pro Ile Arg Phe Pro Phe Gly Phe Thr Trp Pro
 85 90 95

Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His Thr Asp Ser Pro Asp
 100 105 110

Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Ala Thr
 115 120 125

Gln Arg His Leu Thr Val Gly Glu Glu Trp Ser Gln Asp Leu His Ser
 130 135 140

Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr Arg Phe Val Cys Asp Glu
 145 150 155 160

0099559 11290
 105511 6555660

His Tyr Tyr Gly Gly Cys Ser Val Phe Cys Arg Pro Arg Asp Asp	165	170	175
Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly Glu Lys Val Cys Asn	180	185	190
Pro Gly Trp Lys Gly Pro Tyr Cys Thr Glu Pro Ile Cys Leu Pro Gly	195	200	205
Cys Asp Glu Gln His Gly Phe Cys Asp Lys Pro Gly Glu Cys Lys Cys	210	215	220
Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp Glu Cys Ile Arg Tyr Pro	225	230	235
Gly Cys Leu His Gly Thr Cys Gln Gln Pro Trp Gln Cys Asn Cys Gln	245	250	255
Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln Asp Leu Asn Tyr Cys Thr	260	265	270
His His Lys Pro Cys Lys Asn Gly Ala Thr Cys Thr Asn Thr Gly Gln	275	280	285
Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly Tyr Thr Gly Ala Thr Cys	290	295	300
Glu Leu Gly Ile Asp Glu Cys Asp Pro Ser Pro Cys Lys Asn Gly Gly	305	310	315
Ser Cys Thr Asp Leu Glu Asn Ser Tyr Ser Cys Thr Cys Pro Pro Gly	325	330	335
Phe Tyr Gly Lys Ile Cys Glu Leu Ser Ala Met Thr Cys Ala Asp Gly	340	345	350
Pro Cys Phe Asn Gly Gly Arg Cys Ser Asp Ser Pro Asp Gly Gly Tyr	355	360	365
Ser Cys Arg Cys Pro Val Gly Tyr Ser Gly Phe Asn Cys Glu Lys Lys	370	375	380
Ile Asp Tyr Cys Ser Ser Ser Pro Cys Ser Asn Gly Ala Lys Cys Val	385	390	395
Asp Leu Gly Asp Ala Tyr Leu Cys Arg Cys Gln Ala Gly Phe Ser Gly	405	410	415
Arg His Cys Asp Asp Asn Val Asp Asp Cys Ala Ser Ser Pro Cys Ala	420	425	430
Asn Gly Gly Thr Cys Arg Asp Gly Val Asn Asp Phe Ser Cys Thr Cys	435	440	445
Pro Pro Gly Tyr Thr Gly Arg Asn Cys Ser Ala Pro Val Ser Arg Cys	450	455	460

Pro Gly Trp Lys Gly Pro Tyr Cys Thr Glu Pro Ile Cys Leu Pro Gly
195 200 205

Cys 210	Asp	Glu	Gln	His	Gly	Phe	Cys	Asp	Lys	Pro	Gly	Glu	Cys	Lys	Cys
Arg 225	Val	Gly	Trp	Gln	Gly	Arg	Tyr	Cys	Asp	Glu	Cys	Ile	Arg	Tyr	Pro 240
Gly	Cys	Leu	His	Gly	Thr	Cys	Gln	Gln	Pro	Trp	Gln	Cys	Asn	Cys	Gln 255
Glu	Gly	Trp	Gly	Gly	Leu	Phe	Cys	Asn	Gln	Asp	Leu	Asn	Tyr	Cys	Thr
His	His	Lys	Pro	Cys	Lys	Asn	Gly	Ala	Thr	Cys	Thr	Asn	Thr	Gly	Gln
Gly	Ser	Tyr	Thr	Cys	Ser	Cys	Arg	Pro	Gly	Tyr	Thr	Gly	Ala	Thr	Cys
Glu	Leu	Gly	Ile	Asp	Glu	Cys	Asp	Pro	Ser	Pro	Cys	Lys	Asn	Gly	Gly 320
Ser	Cys	Thr	Asp	Leu	Glu	Asn	Ser	Tyr	Ser	Cys	Thr	Cys	Pro	Pro	Gly 335
Phe	Tyr	Gly	Lys	Ile	Cys	Glu	Leu	Ser	Ala	Met	Thr	Cys	Ala	Asp	Gly
Pro	Cys	Phe	Asn	Gly	Gly	Arg	Cys	Ser	Asp	Ser	Pro	Asp	Gly	Gly	Tyr
Ser	Cys	Arg	Cys	Pro	Val	Gly	Tyr	Ser	Gly	Phe	Asn	Cys	Glu	Lys	Lys
Ile	Asp	Tyr	Cys	Ser	Ser	Ser	Pro	Cys	Ser	Asn	Gly	Ala	Lys	Cys	Val 400
Asp	Leu	Gly	Asp	Ala	Tyr	Leu	Cys	Arg	Cys	Gln	Ala	Gly	Phe	Ser	Gly 415
Arg	His	Cys	Asp	Asp	Asn	Val	Asp	Asp	Cys	Ala	Ser	Ser	Pro	Cys	Ala
Asn	Gly	Gly	Thr	Cys	Arg	Asp	Gly	Val	Asn	Asp	Phe	Ser	Cys	Thr	Cys
Pro	Pro	Gly	Tyr	Thr	Gly	Arg	Asn	Cys	Ser	Ala	Pro	Val	Ser	Arg	Cys
Glu	His	Ala	Pro	Cys	His	Asn	Gly	Ala	Thr	Cys	His	Glu	Arg	Gly	His 480
Arg	Tyr	Val	Cys	Glu	Cys	Ala	Arg	Gly	Tyr	Gly	Gly	Pro	Asn	Cys	Gln 495
Phe	Leu	Leu	Pro	Glu	Leu	Pro	Pro	Gly	Pro	Ala	Val	Val	Asp	Leu	Thr

Ser Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala
65 70 75 80

Ser Arg Gly Asn Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala
85 90 95

Trp Pro Arg Ser Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn
100 105 110

Asp Thr Val Gln Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly
115 120 125

Met Ile Asn Pro Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly
130 135 140

Val Ala His Phe Glu Tyr Gln Ile Arg Val Thr Cys Asp Asp Tyr Tyr
145 150 155 160

Tyr Gly Phe Gly Cys Asn Lys Phe Cys Arg Pro Arg Asp Asp Phe Phe
165 170 175

Gly His Tyr Ala Cys Asp Gln Asn Gly Asn Lys Thr Cys Met Glu Gly
180 185 190

Trp Met Gly Pro Glu Cys
195

<210> 6

<211> 1036

<212> PRT

<213> Homo sapiens

<400> 6

Ser Gly Gln Phe Glu Leu Glu Ile Leu Ser Met Gln Asn Val Asn Gly
1 5 10 15

Glu Leu Gln Asn Gly Asn Cys Cys Gly Gly Ala Arg Asn Pro Gly Asp
20 25 30

Arg Lys Cys Thr Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu
35 40 45

Lys Glu Tyr Gln Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly
50 55 60

Ser Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala
65 70 75 80

Ser Arg Gly Asn Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala
85 90 95

Trp Pro Arg Ser Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn
100 105 110

Asp Thr Val Gln Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly
115 120 125

Met Ile Asn Pro Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly
130 135 140

00999999 112901

Val Ala His Phe Glu Tyr Gln Ile Arg Val Thr Cys Asp Asp Tyr Tyr
 145 150 155 160
 Tyr Gly Phe Gly Cys Asn Lys Phe Cys Arg Pro Arg Asp Asp Phe Phe
 165 170 175
 Gly His Tyr Ala Cys Asp Gln Asn Gly Asn Lys Thr Cys Met Glu Gly
 180 185 190
 Trp Met Gly Pro Glu Cys Asn Arg Ala Ile Cys Arg Gln Gly Cys Ser
 195 200 205
 Pro Lys His Gly Ser Cys Lys Leu Pro Gly Asp Cys Arg Cys Gln Tyr
 210 215 220
 Gly Trp Gln Gly Leu Tyr Cys Asp Lys Cys Ile Pro His Pro Gly Cys
 225 230 235 240
 Val His Gly Ile Cys Asn Glu Pro Trp Gln Cys Leu Cys Glu Thr Asn
 245 250 255
 Trp Gly Gly Gln Leu Cys Asp Lys Asp Leu Asn Tyr Cys Gly Thr His
 260 265 270
 Gln Pro Cys Leu Asn Gly Gly Thr Cys Ser Asn Thr Gly Pro Asp Lys
 275 280 285
 Tyr Gln Cys Ser Cys Pro Glu Gly Tyr Ser Gly Pro Asn Cys Glu Ile
 290 295 300
 Ala Glu His Ala Cys Leu Ser Asp Pro Cys His Asn Arg Gly Ser Cys
 305 310 315 320
 Lys Glu Thr Ser Leu Gly Phe Glu Cys Glu Cys Ser Pro Gly Trp Thr
 325 330 335
 Gly Pro Thr Cys Ser Thr Asn Ile Asp Asp Cys Ser Pro Asn Asn Cys
 340 345 350
 Ser His Gly Gly Thr Cys Gln Asp Leu Val Asn Gly Phe Lys Cys Val
 355 360 365
 Cys Pro Pro Gln Trp Thr Gly Lys Thr Cys Gln Leu Asp Ala Asn Glu
 370 375 380
 Cys Glu Ala Lys Pro Cys Val Asn Ala Lys Ser Cys Lys Asn Leu Ile
 385 390 395 400
 Ala Ser Tyr Tyr Cys Asp Cys Leu Pro Gly Trp Met Gly Gln Asn Cys
 405 410 415
 Asp Ile Asn Ile Asn Asp Cys Leu Gly Gln Cys Gln Asn Asp Ala Ser
 420 425 430
 Cys Arg Asp Leu Val Asn Gly Tyr Arg Cys Ile Cys Pro Pro Gly Tyr
 435 440 445

09995593 112904

Ala Gly Asp His Cys Glu Arg Asp Ile Asp Glu Cys Ala Ser Asn Pro
450 455 460

Cys Leu Asn Gly Gly His Cys Gln Asn Glu Ile Asn Arg Phe Gln Cys
465 470 475 480

Leu Cys Pro Thr Gly Phe Ser Gly Asn Leu Cys Gln Leu Asp Ile Asp
485 490 495

Tyr Cys Glu Pro Asn Pro Cys Gln Asn Gly Ala Gln Cys Tyr Asn Arg
500 505 510

Ala Ser Asp Tyr Phe Cys Lys Cys Pro Glu Asp Tyr Glu Gly Lys Asn
515 520 525

Cys Ser His Leu Lys Asp His Cys Arg Thr Thr Pro Cys Glu Val Ile
530 535 540

Asp Ser Cys Thr Val Ala Met Ala Ser Asn Asp Thr Pro Glu Gly Val
545 550 555 560

Arg Tyr Ile Ser Ser Asn Val Cys Gly Pro His Gly Lys Cys Lys Ser
565 570 575

Gln Ser Gly Gly Lys Phe Thr Cys Asp Cys Asn Lys Gly Phe Thr Gly
580 585 590

Thr Tyr Cys His Glu Asn Ile Asn Asp Cys Glu Ser Asn Pro Cys Arg
595 600 605

Asn Gly Gly Thr Cys Ile Asp Gly Val Asn Ser Tyr Lys Cys Ile Cys
610 615 620

Ser Asp Gly Trp Glu Gly Ala Tyr Cys Glu Thr Asn Ile Asn Asp Cys
625 630 635 640

Ser Gln Asn Pro Cys His Asn Gly Gly Thr Cys Arg Asp Leu Val Asn
645 650 655

Asp Phe Tyr Cys Asp Cys Lys Asn Gly Trp Lys Gly Lys Thr Cys His
660 665 670

Ser Arg Asp Ser Gln Cys Asp Glu Ala Thr Cys Asn Asn Gly Gly Thr
675 680 685

Cys Tyr Asp Glu Gly Asp Ala Phe Lys Cys Met Cys Pro Gly Gly Trp
690 695 700

Glu Gly Thr Thr Cys Asn Ile Ala Arg Asn Ser Ser Cys Leu Pro Asn
705 710 715 720

Pro Cys His Asn Gly Gly Thr Cys Val Val Asn Gly Glu Ser Phe Thr
725 730 735

Cys Val Cys Lys Glu Gly Trp Glu Gly Pro Ile Cys Ala Gln Asn Thr
740 745 750

TOB27T 16666666

```
<210> 7
<211> 1187
<212> PRT
```

```

<400> 7
Ser Gly Gln Phe Glu Leu Glu Ile Leu Ser Met Gln Asn Val Asn Gly
  1              5              10              15
Glu Leu Gln Asn Gly Asn Cys Cys Gly Gly Ala Arg Asn Pro Gly Asp
      20              25              30
Arg Lys Cys Thr Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu
      35              40              45
Lys Glu Tyr Gln Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly
      50              55              60
Ser Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala
      65              70              75              80
Ser Arg Gly Asn Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala
      85              90              95
Trp Pro Arg Ser Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn
      100              105              110
Asp Thr Val Gln Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly
      115              120              125
Met Ile Asn Pro Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly
      130              135              140
Val Ala His Phe Glu Tyr Gln Ile Arg Val Thr Cys Asp Asp Tyr Tyr
      145              150              155              160
Tyr Gly Phe Gly Cys Asn Lys Phe Cys Arg Pro Arg Asp Asp Phe Phe
      165              170              175
Gly His Tyr Ala Cys Asp Gln Asn Gly Asn Lys Thr Cys Met Glu Gly
      180              185              190
Trp Met Gly Pro Glu Cys Asn Arg Ala Ile Cys Arg Gln Gly Cys Ser
      195              200              205
Pro Lys His Gly Ser Cys Lys Leu Pro Gly Asp Cys Arg Cys Gln Tyr
      210              215              220
Gly Trp Gln Gly Leu Tyr Cys Asp Lys Cys Ile Pro His Pro Gly Cys
      225              230              235              240
Val His Gly Ile Cys Asn Glu Pro Trp Gln Cys Leu Cys Glu Thr Asn
      245              250              255
Trp Gly Gly Gln Leu Cys Asp Lys Asp Leu Asn Tyr Cys Gly Thr His
      260              265              270
Gln Pro Cys Leu Asn Gly Gly Thr Cys Ser Asn Thr Gly Pro Asp Lys
      275              280              285

```

Tyr	Gln	Cys	Ser	Cys	Pro	Glu	Gly	Tyr	Ser	Gly	Pro	Asn	Cys	Glu	Ile
290						295					300				
Ala	Glu	His	Ala	Cys	Leu	Ser	Asp	Pro	Cys	His	Asn	Arg	Gly	Ser	Cys
305					310					315					320
Lys	Glu	Thr	Ser	Leu	Gly	Phe	Glu	Cys	Glu	Cys	Ser	Pro	Gly	Trp	Thr
				325					330					335	
Gly	Pro	Thr	Cys	Ser	Thr	Asn	Ile	Asp	Asp	Cys	Ser	Pro	Asn	Asn	Cys
			340					345					350		
Ser	His	Gly	Gly	Thr	Cys	Gln	Asp	Leu	Val	Asn	Gly	Phe	Lys	Cys	Val
		355					360					365			
Cys	Pro	Pro	Gln	Trp	Thr	Gly	Lys	Thr	Cys	Gln	Leu	Asp	Ala	Asn	Glu
	370					375					380				
Cys	Glu	Ala	Lys	Pro	Cys	Val	Asn	Ala	Lys	Ser	Cys	Lys	Asn	Leu	Ile
385					390					395					400
Ala	Ser	Tyr	Tyr	Cys	Asp	Cys	Leu	Pro	Gly	Trp	Met	Gly	Gln	Asn	Cys
				405					410					415	
Asp	Ile	Asn	Ile	Asn	Asp	Cys	Leu	Gly	Gln	Cys	Gln	Asn	Asp	Ala	Ser
			420					425					430		
Cys	Arg	Asp	Leu	Val	Asn	Gly	Tyr	Arg	Cys	Ile	Cys	Pro	Pro	Gly	Tyr
		435				440						445			
Ala	Gly	Asp	His	Cys	Glu	Arg	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Asn	Pro
	450					455					460				
Cys	Leu	Asn	Gly	Gly	His	Cys	Gln	Asn	Glu	Ile	Asn	Arg	Phe	Gln	Cys
465					470					475					480
Leu	Cys	Pro	Thr	Gly	Phe	Ser	Gly	Asn	Leu	Cys	Gln	Leu	Asp	Ile	Asp
				485					490					495	
Tyr	Cys	Glu	Pro	Asn	Pro	Cys	Gln	Asn	Gly	Ala	Gln	Cys	Tyr	Asn	Arg
			500					505					510		
Ala	Ser	Asp	Tyr	Phe	Cys	Lys	Cys	Pro	Glu	Asp	Tyr	Glu	Gly	Lys	Asn
		515					520					525			
Cys	Ser	His	Leu	Lys	Asp	His	Cys	Arg	Thr	Thr	Pro	Cys	Glu	Val	Ile
	530					535					540				
Asp	Ser	Cys	Thr	Val	Ala	Met	Ala	Ser	Asn	Asp	Thr	Pro	Glu	Gly	Val
545					550					555					560
Arg	Tyr	Ile	Ser	Ser	Asn	Val	Cys	Gly	Pro	His	Gly	Lys	Cys	Lys	Ser
				565					570					575	
Gln	Ser	Gly	Gly	Lys	Phe	Thr	Cys	Asp	Cys	Asn	Lys	Gly	Phe	Thr	Gly
			580					585					590		

Thr	Tyr	Cys	His	Glu	Asn	Ile	Asn	Asp	Cys	Glu	Ser	Asn	Pro	Cys	Arg	
		595						600					605			
Asn	Gly	Gly	Thr	Cys	Ile	Asp	Gly	Val	Asn	Ser	Tyr	Lys	Cys	Ile	Cys	
	610					615					620					
Ser	Asp	Gly	Trp	Glu	Gly	Ala	Tyr	Cys	Glu	Thr	Asn	Ile	Asn	Asp	Cys	
625					630					635					640	
Ser	Gln	Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Arg	Asp	Leu	Val	Asn	
				645					650					655		
Asp	Phe	Tyr	Cys	Asp	Cys	Lys	Asn	Gly	Trp	Lys	Gly	Lys	Thr	Cys	His	
			660					665					670			
Ser	Arg	Asp	Ser	Gln	Cys	Asp	Glu	Ala	Thr	Cys	Asn	Asn	Gly	Gly	Thr	
		675					680					685				
Cys	Tyr	Asp	Glu	Gly	Asp	Ala	Phe	Lys	Cys	Met	Cys	Pro	Gly	Gly	Trp	
	690					695					700					
Glu	Gly	Thr	Thr	Cys	Asn	Ile	Ala	Arg	Asn	Ser	Ser	Cys	Leu	Pro	Asn	
705					710					715					720	
Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Val	Val	Asn	Gly	Glu	Ser	Phe	Thr	
				725					730					735		
Cys	Val	Cys	Lys	Glu	Gly	Trp	Glu	Gly	Pro	Ile	Cys	Ala	Gln	Asn	Thr	
			740					745					750			
Asn	Asp	Cys	Ser	Pro	His	Pro	Cys	Tyr	Asn	Ser	Gly	Thr	Cys	Val	Asp	
		755					760					765				
Gly	Asp	Asn	Trp	Tyr	Arg	Cys	Glu	Cys	Ala	Pro	Gly	Phe	Ala	Gly	Pro	
	770					775					780					
Asp	Cys	Arg	Ile	Asn	Ile	Asn	Glu	Cys	Gln	Ser	Ser	Pro	Cys	Ala	Phe	
785					790					795					800	
Gly	Ala	Thr	Cys	Val	Asp	Glu	Ile	Asn	Gly	Tyr	Arg	Cys	Val	Cys	Pro	
				805					810					815		
Pro	Gly	His	Ser	Gly	Ala	Lys	Cys	Gln	Glu	Val	Ser	Gly	Arg	Pro	Cys	
			820					825					830			
Ile	Thr	Met	Gly	Ser	Val	Ile	Pro	Asp	Gly	Ala	Lys	Trp	Asp	Asp	Asp	
		835					840					845				
Cys	Asn	Thr	Cys	Gln	Cys	Leu	Asn	Gly	Arg	Ile	Ala	Cys	Ser	Lys	Val	
	850					855					860					
Trp	Cys	Gly	Pro	Arg	Pro	Cys	Leu	Leu	His	Lys	Gly	His	Ser	Glu	Cys	
865					870					875					880	
Pro	Ser	Gly	Gln	Ser	Cys	Ile	Pro	Ile	Leu	Asp	Asp	Gln	Cys	Phe	Val	
				885					890						895	

[illegible]

<213> Homo sapiens

<223> Description of Combined DNA/RNA Molecule: cDNA to mRNA, and amino acid

<222> (179) .. (2347)

aca gat tct cct gat gac ctc gca aca gaa aac cca gaa aga ctc atc 610
Thr Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile
130 135 140

agc cgc ctg gcc acc cag agg cac ctg acg gtg ggc gag gag tgg tcc	658
Ser Arg Leu Ala Thr Gln Arg His Leu Thr Val Gly Glu Glu Trp Ser	
145 150 155 160	
cag gac ctg cac agc agc ggc cgc acg gac ctc aag tac tcc tac cgc	706
Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr Arg	
165 170 175	
ttc gtg tgt gac gaa cac tac tac gga gag ggc tgc tcc gtt ttc tgc	754
Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys	
180 185 190	
cgt ccc cgg gac gat gcc ttc ggc cac ttc acc tgt ggg gag cgt ggg	802
Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly	
195 200 205	
gag aaa gtg tgc aac cct ggc tgg aaa ggg ccc tac tgc aca gag ccg	850
Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys Thr Glu Pro	
210 215 220	
atc tgc ctg cct gga tgt gat gag cag cat gga ttt tgt gac aaa cca	898
Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys Asp Lys Pro	
225 230 235 240	
ggg gaa tgc aag tgc aga gtg ggc tgg cag ggc cgg tac tgt gac gag	946
Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp Glu	
245 250 255	
tgt atc cgc tat cca ggc tgt ctc cat ggc acc tgc cag cag ccc tgg	994
Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln Pro Trp	
260 265 270	
cag tgc aac tgc cag gaa ggc tgg ggg ggc ctt ttc tgc aac cag gac	1042
Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln Asp	
275 280 285	
ctg aac tac tgc aca cac cat aag ccc tgc aag aat gga gcc acc tgc	1090
Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly Ala Thr Cys	
290 295 300	
acc aac acg ggc cag ggg agc tac act tgc tct tgc cgg cct ggg tac	1138
Thr Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly Tyr	
305 310 315 320	
aca ggt gcc acc tgc gag ctg ggg att gac gag tgt gac ccc agc cct	1186
Thr Gly Ala Thr Cys Glu Leu Gly Ile Asp Glu Cys Asp Pro Ser Pro	
325 330 335	
tgt aag aac gga ggg agc tgc acg gat ctc gag aac agc tac tcc tgt	1234
Cys Lys Asn Gly Gly Ser Cys Thr Asp Leu Glu Asn Ser Tyr Ser Cys	
340 345 350	
acc tgc cca ccc ggc ttc tac ggc aaa atc tgt gaa ttg agt gcc atg	1282
Thr Cys Pro Pro Gly Phe Tyr Gly Lys Ile Cys Glu Leu Ser Ala Met	
355 360 365	

acc tgt gcg gac ggc cct tgc ttt aac ggg ggt cgg tgc tca gac agc 1330
 Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Ser Asp Ser
 370 375 380

ccc gat gga ggg tac agc tgc cgc tgc ccc gtg ggc tac tcc ggc ttc 1378
 Pro Asp Gly Gly Tyr Ser Cys Arg Cys Pro Val Gly Tyr Ser Gly Phe
 385 390 395 400

aac tgt gag aag aaa att gac tac tgc agc tct tca ccc tgt tct aat 1426
 Asn Cys Glu Lys Lys Ile Asp Tyr Cys Ser Ser Ser Pro Cys Ser Asn
 405 410 415

ggg gcc aag tgt gtg gac ctc ggt gat gcc tac ctg tgc cgc tgc cag 1474
 Gly Ala Lys Cys Val Asp Leu Gly Asp Ala Tyr Leu Cys Arg Cys Gln
 420 425 430

gcc ggc ttc tcg ggg agg cac tgt gac gac aac gtg gac gac tgc gcc 1522
 Ala Gly Phe Ser Gly Arg His Cys Asp Asp Asn Val Asp Asp Cys Ala
 435 440 445

tcc tcc ccg tgc gcc aac ggg ggc acc tgc cgg gat ggc gtg aac gac 1570
 Ser Ser Pro Cys Ala Asn Gly Gly Thr Cys Arg Asp Gly Val Asn Asp
 450 455 460

ttc tcc tgc acc tgc ccg cct ggc tac acg ggc agg aac tgc agt gcc 1618
 Phe Ser Cys Thr Cys Pro Pro Gly Tyr Thr Gly Arg Asn Cys Ser Ala
 465 470 475 480

ccc gtc agc agg tgc gag cac gca ccc tgc cac aat ggg gcc acc tgc 1666
 Pro Val Ser Arg Cys Glu His Ala Pro Cys His Asn Gly Ala Thr Cys
 485 490 495

cac gag agg ggc cac cgc tat gtg tgc gag tgt gcc cga ggc tac ggg 1714
 His Glu Arg Gly His Arg Tyr Val Cys Glu Cys Ala Arg Gly Tyr Gly
 500 505 510

ggg ccc aac tgc cag ttc ctg ctc ccc gag ctg ccc ccg ggc cca gcg 1762
 Gly Pro Asn Cys Gln Phe Leu Leu Pro Glu Leu Pro Pro Gly Pro Ala
 515 520 525

gtg gtg gac ctc act gag aag cta gag ggc cag ggc ggg cca ttc ccc 1810
 Val Val Asp Leu Thr Glu Lys Leu Glu Gly Gln Gly Gly Pro Phe Pro
 530 535 540

tgg gtg gcc gtg tgc gcc ggg gtc atc ctt gtc ctc atg ctg ctg ctg 1858
 Trp Val Ala Val Cys Ala Gly Val Ile Leu Val Leu Met Leu Leu Leu
 545 550 555 560

ggc tgt gcc gct gtg gtg gtc tgc gtc cgg ctg agg ctg cag aag cac 1906
 Gly Cys Ala Ala Val Val Val Cys Val Arg Leu Arg Leu Gln Lys His
 565 570 575

cgg ccc cca gcc gac ccc tgc cgg ggg gag acg gag acc atg aac aac 1954
 Arg Pro Pro Ala Asp Pro Cys Arg Gly Glu Thr Glu Thr Met Asn Asn
 580 585 590

```

ctg gcc aac tgc cag cgt gag aag gac atc tca gtc agc atc atc ggg 2002
Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Val Ser Ile Ile Gly
      595                      600                      605

gcc acg cag atc aag aac acc aac aag aag gcg gac ttc cac ggg gac 2050
Ala Thr Gln Ile Lys Asn Thr Asn Lys Lys Ala Asp Phe His Gly Asp
      610                      615                      620

cac agc gcc gac aag aat ggc ttc aag gcc cgc tac cca gcg gtg gac 2098
His Ser Ala Asp Lys Asn Gly Phe Lys Ala Arg Tyr Pro Ala Val Asp
      625                      630                      635                      640

tat aac ctc gtg cag gac ctc aag ggt gac gac acc gcc gtc agg gac 2146
Tyr Asn Leu Val Gln Asp Leu Lys Gly Asp Asp Thr Ala Val Arg Asp
      645                      650                      655

gcg cac agc aag cgt gac acc aag tgc cag ccc cag ggc tcc tca ggg 2194
Ala His Ser Lys Arg Asp Thr Lys Cys Gln Pro Gln Gly Ser Ser Gly
      660                      665                      670

gag gag aag ggg acc ccg acc aca ctc agg ggt gga gaa gca tct gaa 2242
Glu Glu Lys Gly Thr Pro Thr Thr Leu Arg Gly Gly Glu Ala Ser Glu
      675                      680                      685

aga aaa agg ccg gac tcg ggc tgt tca act tca aaa gac acc aag tac 2290
Arg Lys Arg Pro Asp Ser Gly Cys Ser Thr Ser Lys Asp Thr Lys Tyr
      690                      695                      700

cag tcg gtg tac gtc ata tcc gag gag aag gat gag tgc gtc ata gca 2338
Gln Ser Val Tyr Val Ile Ser Glu Glu Lys Asp Glu Cys Val Ile Ala
      705                      710                      715                      720

act gag gtg taaaatggaa gtgagatggc aagactcccg tttctcttaa 2387
Thr Glu Val

aataagtaaa attccaagga tatatgcccc aacgaatgct gctgaagagg agggaggcct 2447

cgtggactgc tgctgagaaa ccgagttcag accgagcagg ttctcctcct gaggtcctcg 2507

acgcctgccg acagcctgtc ggggcccggc cgcttgccgc actgccttcc gtgacgtcgc 2567

cgttgcacta tggacagttg ctcttaagag aatatatatt taaatgggtg aactgaatta 2627

cgcataagaa gcatgcactg cctgagtgta tatttt 2663

<210> 9
<211> 723
<212> PRT
<213> Homo sapiens

<400> 9
Met Gly Ser Arg Cys Ala Leu Ala Leu Ala Val Leu Ser Ala Leu Leu
  1                      5                      10                      15

Cys Gln Val Trp Ser Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe
  20                      25                      30

```

Val	Asn	Lys	Lys	Gly	Leu	Leu	Gly	Asn	Arg	Asn	Cys	Cys	Arg	Gly	Gly	
		35					40								45	
Ala	Gly	Pro	Pro	Pro	Cys	Ala	Cys	Arg	Thr	Phe	Phe	Arg	Val	Cys	Leu	
	50					55					60					
Lys	His	Tyr	Gln	Ala	Ser	Val	Ser	Pro	Glu	Pro	Pro	Cys	Thr	Tyr	Gly	
	65				70					75					80	
Ser	Ala	Val	Thr	Pro	Val	Leu	Gly	Val	Asp	Ser	Phe	Ser	Leu	Pro	Asp	
				85					90					95		
Gly	Gly	Gly	Ala	Asp	Ser	Ala	Phe	Ser	Asn	Pro	Ile	Arg	Phe	Pro	Phe	
			100					105					110			
Gly	Phe	Thr	Trp	Pro	Gly	Thr	Phe	Ser	Leu	Ile	Ile	Glu	Ala	Leu	His	
		115					120					125				
Thr	Asp	Ser	Pro	Asp	Asp	Leu	Ala	Thr	Glu	Asn	Pro	Glu	Arg	Leu	Ile	
	130					135					140					
Ser	Arg	Leu	Ala	Thr	Gln	Arg	His	Leu	Thr	Val	Gly	Glu	Glu	Trp	Ser	
	145				150					155					160	
Gln	Asp	Leu	His	Ser	Ser	Gly	Arg	Thr	Asp	Leu	Lys	Tyr	Ser	Tyr	Arg	
				165					170					175		
Phe	Val	Cys	Asp	Glu	His	Tyr	Tyr	Gly	Glu	Gly	Cys	Ser	Val	Phe	Cys	
			180					185					190			
Arg	Pro	Arg	Asp	Asp	Ala	Phe	Gly	His	Phe	Thr	Cys	Gly	Glu	Arg	Gly	
		195					200					205				
Glu	Lys	Val	Cys	Asn	Pro	Gly	Trp	Lys	Gly	Pro	Tyr	Cys	Thr	Glu	Pro	
	210					215					220					
Ile	Cys	Leu	Pro	Gly	Cys	Asp	Glu	Gln	His	Gly	Phe	Cys	Asp	Lys	Pro	
	225				230					235					240	
Gly	Glu	Cys	Lys	Cys	Arg	Val	Gly	Trp	Gln	Gly	Arg	Tyr	Cys	Asp	Glu	
				245					250					255		
Cys	Ile	Arg	Tyr	Pro	Gly	Cys	Leu	His	Gly	Thr	Cys	Gln	Gln	Pro	Trp	
		260						265					270			
Gln	Cys	Asn	Cys	Gln	Glu	Gly	Trp	Gly	Gly	Leu	Phe	Cys	Asn	Gln	Asp	
		275					280					285				
Leu	Asn	Tyr	Cys	Thr	His	His	Lys	Pro	Cys	Lys	Asn	Gly	Ala	Thr	Cys	
	290					295					300					
Thr	Asn	Thr	Gly	Gln	Gly	Ser	Tyr	Thr	Cys	Ser	Cys	Arg	Pro	Gly	Tyr	
	305				310					315					320	
Thr	Gly	Ala	Thr	Cys	Glu	Leu	Gly	Ile	Asp	Glu	Cys	Asp	Pro	Ser	Pro	
				325					330						335	

Cys Lys Asn Gly Gly Ser Cys Thr Asp Leu Glu Asn Ser Tyr Ser Cys
 340 345 350
 Thr Cys Pro Pro Gly Phe Tyr Gly Lys Ile Cys Glu Leu Ser Ala Met
 355 360 365
 Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Ser Asp Ser
 370 375 380
 Pro Asp Gly Gly Tyr Ser Cys Arg Cys Pro Val Gly Tyr Ser Gly Phe
 385 390 395 400
 Asn Cys Glu Lys Lys Ile Asp Tyr Cys Ser Ser Ser Pro Cys Ser Asn
 405 410 415
 Gly Ala Lys Cys Val Asp Leu Gly Asp Ala Tyr Leu Cys Arg Cys Gln
 420 425 430
 Ala Gly Phe Ser Gly Arg His Cys Asp Asp Asn Val Asp Asp Cys Ala
 435 440 445
 Ser Ser Pro Cys Ala Asn Gly Gly Thr Cys Arg Asp Gly Val Asn Asp
 450 455 460
 Phe Ser Cys Thr Cys Pro Pro Gly Tyr Thr Gly Arg Asn Cys Ser Ala
 465 470 475 480
 Pro Val Ser Arg Cys Glu His Ala Pro Cys His Asn Gly Ala Thr Cys
 485 490 495
 His Glu Arg Gly His Arg Tyr Val Cys Glu Cys Ala Arg Gly Tyr Gly
 500 505 510
 Gly Pro Asn Cys Gln Phe Leu Leu Pro Glu Leu Pro Pro Gly Pro Ala
 515 520 525
 Val Val Asp Leu Thr Glu Lys Leu Glu Gly Gln Gly Gly Pro Phe Pro
 530 535 540
 Trp Val Ala Val Cys Ala Gly Val Ile Leu Val Leu Met Leu Leu Leu
 545 550 555 560
 Gly Cys Ala Ala Val Val Val Cys Val Arg Leu Arg Leu Gln Lys His
 565 570 575
 Arg Pro Pro Ala Asp Pro Cys Arg Gly Glu Thr Glu Thr Met Asn Asn
 580 585 590
 Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Val Ser Ile Ile Gly
 595 600 605
 Ala Thr Gln Ile Lys Asn Thr Asn Lys Lys Ala Asp Phe His Gly Asp
 610 615 620
 His Ser Ala Asp Lys Asn Gly Phe Lys Ala Arg Tyr Pro Ala Val Asp
 625 630 635 640

0309593
 T0627 E655650

```

<210> 10
<211> 4208
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (409)..(4062)

<400> 10
ggccggcccg cgagctaggc tggttttttt ttttctcccc tccctcccc ctttttccat 60
gcagctgatc taaaagggaa taaaaggctg cgcataatca taataataaa agaaggggag 120
cgcgagagaaa ggaaagaaa cggggagggtg gaagaggagg gggagcgtct caaagaagcg 180
atcagaataa taaaaggagg ccgggctctt tgccttctgg aacgggccgc tcttgaaagg 240
gcttttgaaa agtgggtgtt ttttccagtc gtgcatgctc caatcggcgg agtatattag 300
agccggggacg cggcgggccgc aggggcagcg gcgacggcag caccggcggc agcaccagcg 360
cgaacagcag cggcggcgtc ccgagtgcc gcggcgcgcg gcgcagcg atg cgt tcc 417
                                     Met Arg Ser
                                     1

cca cgg acg cgc ggc cgg tcc ggg cgc ccc cta agc ctc ctg ctc gcc 465
Pro Arg Thr Arg Gly Arg Ser Gly Arg Pro Leu Ser Leu Leu Leu Ala
      5                10                15

ctg ctc tgt gcc ctg cga gcc aag gtg tgt ggg gcc tcg ggt cag ttc 513
Leu Leu Cys Ala Leu Arg Ala Lys Val Cys Gly Ala Ser Gly Gln Phe
      20                25                30                35

gag ttg gag atc ctg tcc atg cag aac gtg aac ggg gag ctg cag aac 561
Glu Leu Glu Ile Leu Ser Met Gln Asn Val Asn Gly Glu Leu Gln Asn
      40                45                50

```

ggg aac tgc tgc ggc ggc gcc cgg aac ccg gga gac cgc aag tgc acc Gly Asn Cys Cys Gly Gly Ala Arg Asn Pro Gly Asp Arg Lys Cys Thr	609
55 60 65	
cgc gac gag tgt gac aca tac ttc aaa gtg tgc ctc aag gag tat cag Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu Lys Glu Tyr Gln	657
70 75 80	
tcc cgc gtc acg gcc ggg ggg ccc tgc agc ttc ggc tca ggg tcc acg Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly Ser Gly Ser Thr	705
85 90 95	
cct gtc atc ggg ggc aac acc ttc aac ctc aag gcc agc cgc ggc aac Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala Ser Arg Gly Asn	753
100 105 110 115	
gac cgc aac cgc atc gtg ctg cct ttc agt ttc gcc tgg ccg agg tcc Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala Trp Pro Arg Ser	801
120 125 130	
tat acg ttg ctt gtg gag gcg tgg gat tcc agt aat gac acc gtt caa Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn Asp Thr Val Gln	849
135 140 145	
cct gac agt att att gaa aag gct tct cac tcg ggc atg atc aac ccc Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly Met Ile Asn Pro	897
150 155 160	
agc cgg cag tgg cag acg ctg aag cag aac acg ggc gtt gcc cac ttt Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly Val Ala His Phe	945
165 170 175	
gag tat cag atc cgc gtg acc tgt gat gac tac tac tat ggc ttt ggc Glu Tyr Gln Ile Arg Val Thr Cys Asp Asp Tyr Tyr Tyr Gly Phe Gly	993
180 185 190 195	
tgc aat aag ttc tgc cgc ccc aga gat gac ttc ttt gga cac tat gcc Cys Asn Lys Phe Cys Arg Pro Arg Asp Asp Phe Phe Gly His Tyr Ala	1041
200 205 210	
tgt gac cag aat ggc aac aaa act tgc atg gaa ggc tgg atg ggc ccc Cys Asp Gln Asn Gly Asn Lys Thr Cys Met Glu Gly Trp Met Gly Pro	1089
215 220 225	
gaa tgt aac aga gct att tgc cga caa ggc tgc agt cct aag cat ggg Glu Cys Asn Arg Ala Ile Cys Arg Gln Gly Cys Ser Pro Lys His Gly	1137
230 235 240	
tct tgc aaa ctc cca ggt gac tgc agg tgc cag tac ggc tgg caa ggc Ser Cys Lys Leu Pro Gly Asp Cys Arg Cys Gln Tyr Gly Trp Gln Gly	1185
245 250 255	
ctg tac tgt gat aag tgc atc cca cac ccg gga tgc gtc cac ggc atc Leu Tyr Cys Asp Lys Cys Ile Pro His Pro Gly Cys Val His Gly Ile	1233
260 265 270 275	

tgt aat gag ccc tgg cag tgc ctc tgt gag acc aac tgg ggc ggc cag 1281
 Cys Asn Glu Pro Trp Gln Cys Leu Cys Glu Thr Asn Trp Gly Gly Gln
 280 285 290

ctc tgt gac aaa gat ctc aat tac tgt ggg act cat cag ccg tgt ctc 1329
 Leu Cys Asp Lys Asp Leu Asn Tyr Cys Gly Thr His Gln Pro Cys Leu
 295 300 305

aac ggg gga act tgt agc aac aca ggc cct gac aaa tat cag tgt tcc 1377
 Asn Gly Gly Thr Cys Ser Asn Thr Gly Pro Asp Lys Tyr Gln Cys Ser
 310 315 320

tgc cct gag ggg tat tca gga ccc aac tgt gaa att gct gag cac gcc 1425
 Cys Pro Glu Gly Tyr Ser Gly Pro Asn Cys Glu Ile Ala Glu His Ala
 325 330 335

tgc ctc tct gat ccc tgt cac aac aga ggc agc tgt aag gag acc tcc 1473
 Cys Leu Ser Asp Pro Cys His Asn Arg Gly Ser Cys Lys Glu Thr Ser
 340 345 350 355

ctg ggc ttt gag tgt gag tgt tcc cca ggc tgg acc ggc ccc aca tgc 1521
 Leu Gly Phe Glu Cys Glu Cys Ser Pro Gly Trp Thr Gly Pro Thr Cys
 360 365 370

tct aca aac att gat gac tgt tct cct aat aac tgt tcc cac ggg ggc 1569
 Ser Thr Asn Ile Asp Asp Cys Ser Pro Asn Asn Cys Ser His Gly Gly
 375 380 385

acc tgc cag gac ctg gtt aac gga ttt aag tgt gtg tgc ccc cca cag 1617
 Thr Cys Gln Asp Leu Val Asn Gly Phe Lys Cys Val Cys Pro Pro Gln
 390 395 400

tgg act ggg aaa acg tgc cag tta gat gca aat gaa tgt gag gcc aaa 1665
 Trp Thr Gly Lys Thr Cys Gln Leu Asp Ala Asn Glu Cys Glu Ala Lys
 405 410 415

cct tgt gta aac gcc aaa tcc tgt aag aat ctc att gcc agc tac tac 1713
 Pro Cys Val Asn Ala Lys Ser Cys Lys Asn Leu Ile Ala Ser Tyr Tyr
 420 425 430 435

tgc gac tgt ctt ccc ggc tgg atg ggt cag aat tgt gac ata aat att 1761
 Cys Asp Cys Leu Pro Gly Trp Met Gly Gln Asn Cys Asp Ile Asn Ile
 440 445 450

aat gac tgc ctt ggc cag tgt cag aat gac gcc tcc tgt cgg gat ttg 1809
 Asn Asp Cys Leu Gly Gln Cys Gln Asn Asp Ala Ser Cys Arg Asp Leu
 455 460 465

gtt aat ggt tat cgc tgt atc tgt cca cct ggc tat gca ggc gat cac 1857
 Val Asn Gly Tyr Arg Cys Ile Cys Pro Pro Gly Tyr Ala Gly Asp His
 470 475 480

tgt gag aga gac atc gat gaa tgt gcc agc aac ccc tgt ttg aat ggg 1905
 Cys Glu Arg Asp Ile Asp Glu Cys Ala Ser Asn Pro Cys Leu Asn Gly
 485 490 495

T062T E6555550

ggt cac tgt cag aat gaa atc aac aga ttc cag tgt ctg tgt ccc act	1953
Gly His Cys Gln Asn Glu Ile Asn Arg Phe Gln Cys Leu Cys Pro Thr	
500 505 510 515	
ggt ttc tct gga aac ctc tgt cag ctg gac atc gat tat tgt gag cct	2001
Gly Phe Ser Gly Asn Leu Cys Gln Leu Asp Ile Asp Tyr Cys Glu Pro	
520 525 530	
aat ccc tgc cag aac ggt gcc cag tgc tac aac cgt gcc agt gac tat	2049
Asn Pro Cys Gln Asn Gly Ala Gln Cys Tyr Asn Arg Ala Ser Asp Tyr	
535 540 545	
ttc tgc aag tgc ccc gag gac tat gag ggc aag aac tgc tca cac ctg	2097
Phe Cys Lys Cys Pro Glu Asp Tyr Glu Gly Lys Asn Cys Ser His Leu	
550 555 560	
aaa gac cac tgc cgc acg acc ccc tgt gaa gtg att gac agc tgc aca	2145
Lys Asp His Cys Arg Thr Thr Pro Cys Glu Val Ile Asp Ser Cys Thr	
565 570 575	
gtg gcc atg gct tcc aac gac aca cct gaa ggg gtg cgg tat att tcc	2193
Val Ala Met Ala Ser Asn Asp Thr Pro Glu Gly Val Arg Tyr Ile Ser	
580 585 590 595	
tcc aac gtc tgt ggt cct cac ggg aag tgc aag agt cag tgc gga ggc	2241
Ser Asn Val Cys Gly Pro His Gly Lys Cys Lys Ser Gln Ser Gly Gly	
600 605 610	
aaa ttc acc tgt gac tgt aac aaa ggc ttc acg gga aca tac tgc cat	2289
Lys Phe Thr Cys Asp Cys Asn Lys Gly Phe Thr Gly Thr Tyr Cys His	
615 620 625	
gaa aat att aat gac tgt gag agc aac cct tgt aga aac ggt ggc act	2337
Glu Asn Ile Asn Asp Cys Glu Ser Asn Pro Cys Arg Asn Gly Gly Thr	
630 635 640	
tgc atc gat ggt gtc aac tcc tac aag tgc atc tgt agt gac ggc tgg	2385
Cys Ile Asp Gly Val Asn Ser Tyr Lys Cys Ile Cys Ser Asp Gly Trp	
645 650 655	
gag ggg gcc tac tgt gaa acc aat att aat gac tgc agc cag aac ccc	2433
Glu Gly Ala Tyr Cys Glu Thr Asn Ile Asn Asp Cys Ser Gln Asn Pro	
660 665 670 675	
tgc cac aat ggg ggc acg tgt cgc gac ctg gtc aat gac ttc tac tgt	2481
Cys His Asn Gly Gly Thr Cys Arg Asp Leu Val Asn Asp Phe Tyr Cys	
680 685 690	
gac tgt aaa aat ggg tgg aaa gga aag acc tgc cac tca cgt gac agt	2529
Asp Cys Lys Asn Gly Trp Lys Gly Lys Thr Cys His Ser Arg Asp Ser	
695 700 705	
cag tgt gat gag gcc acg tgc aac aac ggt ggc acc tgc tat gat gag	2577
Gln Cys Asp Glu Ala Thr Cys Asn Asn Gly Gly Thr Cys Tyr Asp Glu	
710 715 720	

00995593 112901
106211 E6555550

ggg gat gct ttt aag tgc atg tgt cct ggc ggc tgg gaa gga aca acc	2625
Gly Asp Ala Phe Lys Cys Met Cys Pro Gly Gly Trp Glu Gly Thr Thr	
725 730 735	
tgt aac ata gcc cga aac agt agc tgc ctg ccc aac ccc tgc cat aat	2673
Cys Asn Ile Ala Arg Asn Ser Ser Cys Leu Pro Asn Pro Cys His Asn	
740 745 750 755	
ggg ggc aca tgt gtg gtc aac ggc gag tcc ttt acg tgc gtc tgc aag	2721
Gly Gly Thr Cys Val Val Asn Gly Glu Ser Phe Thr Cys Val Cys Lys	
760 765 770	
gaa ggc tgg gag ggg ccc atc tgt gct cag aat acc aat gac tgc agc	2769
Glu Gly Trp Glu Gly Pro Ile Cys Ala Gln Asn Thr Asn Asp Cys Ser	
775 780 785	
cct cat ccc tgt tac aac agc ggc acc tgt gtg gat gga gac aac tgg	2817
Pro His Pro Cys Tyr Asn Ser Gly Thr Cys Val Asp Gly Asp Asn Trp	
790 795 800	
tac cgg tgc gaa tgt gcc ccg ggt ttt gct ggg ccc gac tgc aga ata	2865
Tyr Arg Cys Glu Cys Ala Pro Gly Phe Ala Gly Pro Asp Cys Arg Ile	
805 810 815	
aac atc aat gaa tgc cag tct tca cct tgt gcc ttt gga gcg acc tgt	2913
Asn Ile Asn Glu Cys Gln Ser Ser Pro Cys Ala Phe Gly Ala Thr Cys	
820 825 830 835	
gtg gat gag atc aat ggc tac cgg tgt gtc tgc cct cca ggg cac agt	2961
Val Asp Glu Ile Asn Gly Tyr Arg Cys Val Cys Pro Pro Gly His Ser	
840 845 850	
ggg gcc aag tgc cag gaa gtt tca ggg aga cct tgc atc acc atg ggg	3009
Gly Ala Lys Cys Gln Glu Val Ser Gly Arg Pro Cys Ile Thr Met Gly	
855 860 865	
agt gtg ata cca gat ggg gcc aaa tgg gat gat gac tgt aat acc tgc	3057
Ser Val Ile Pro Asp Gly Ala Lys Trp Asp Asp Asp Cys Asn Thr Cys	
870 875 880	
cag tgc ctg aat gga cgg atc gcc tgc tca aag gtc tgg tgt ggc cct	3105
Gln Cys Leu Asn Gly Arg Ile Ala Cys Ser Lys Val Trp Cys Gly Pro	
885 890 895	
cga cct tgc ctg ctc cac aaa ggg cac agc gag tgc ccc agc ggg cag	3153
Arg Pro Cys Leu Leu His Lys Gly His Ser Glu Cys Pro Ser Gly Gln	
900 905 910 915	
agc tgc atc ccc atc ctg gac gac cag tgc ttc gtc cac ccc tgc act	3201
Ser Cys Ile Pro Ile Leu Asp Asp Gln Cys Phe Val His Pro Cys Thr	
920 925 930	
ggg gtg ggc gag tgt cgg tct tcc agt ctc cag ccg gtg aag aca aag	3249
Gly Val Gly Glu Cys Arg Ser Ser Ser Leu Gln Pro Val Lys Thr Lys	
935 940 945	

tgc acc tct gac tcc tat tac cag gat aac tgt gcg aac atc aca ttt	3297
Cys Thr Ser Asp Ser Tyr Tyr Gln Asp Asn Cys Ala Asn Ile Thr Phe	
950 955 960	
acc ttt aac aag gag atg atg tca cca ggt ctt act acg gag cac att	3345
Thr Phe Asn Lys Glu Met Met Ser Pro Gly Leu Thr Thr Glu His Ile	
965 970 975	
tgc agt gaa ttg agg aat ttg aat att ttg aag aat gtt tcc gct gaa	3393
Cys Ser Glu Leu Arg Asn Leu Asn Ile Leu Lys Asn Val Ser Ala Glu	
980 985 990 995	
tat tca atc tac atc gct tgc gag cct tcc cct tca gcg aac aat gaa	3441
Tyr Ser Ile Tyr Ile Ala Cys Glu Pro Ser Pro Ser Ala Asn Asn Glu	
1000 1005 1010	
ata cat gtg gcc att tct gct gaa gat ata cgg gat gat ggg aac ccg	3489
Ile His Val Ala Ile Ser Ala Glu Asp Ile Arg Asp Asp Gly Asn Pro	
1015 1020 1025	
atc aag gaa atc act gac aaa ata atc gat ctt gtt agt aaa cgt gat	3537
Ile Lys Glu Ile Thr Asp Lys Ile Ile Asp Leu Val Ser Lys Arg Asp	
1030 1035 1040	
gga aac agc tcg ctg att gct gcc gtt gca gaa gta aga gtt cag agg	3585
Gly Asn Ser Ser Leu Ile Ala Ala Val Ala Glu Val Arg Val Gln Arg	
1045 1050 1055	
cgg cct ctg aag aac aga aca gat ttc ctt gtt ccc ttg ctg agc tct	3633
Arg Pro Leu Lys Asn Arg Thr Asp Phe Leu Val Pro Leu Leu Ser Ser	
1060 1065 1070 1075	
gtc tta act gtg gct tgg atc tgt tgc ttg gtg acg gcc ttc tac tgg	3681
Val Leu Thr Val Ala Trp Ile Cys Cys Leu Val Thr Ala Phe Tyr Trp	
1080 1085 1090	
tgc ctg cgg aag cgg cgg aag cgg gcc agc cac aca cac tca gcc tct	3729
Cys Leu Arg Lys Arg Arg Lys Pro Gly Ser His Thr His Ser Ala Ser	
1095 1100 1105	
gag gac aac acc acc aac aac gtg cgg gag cag ctg aac cag atc aaa	3777
Glu Asp Asn Thr Thr Asn Asn Val Arg Glu Gln Leu Asn Gln Ile Lys	
1110 1115 1120	
aac ccc att gag aaa cat ggg gcc aac acg gtc ccc atc aag gat tat	3825
Asn Pro Ile Glu Lys His Gly Ala Asn Thr Val Pro Ile Lys Asp Tyr	
1125 1130 1135	
gag aac aag aac tcc aaa atg tct aaa ata agg aca cac aat tct gaa	3873
Glu Asn Lys Asn Ser Lys Met Ser Lys Ile Arg Thr His Asn Ser Glu	
1140 1145 1150 1155	
gta gaa gag gac gac atg gac aaa cac cag cag aaa gcc cgg ttt gcc	3921
Val Glu Glu Asp Asp Met Asp Lys His Gln Gln Lys Ala Arg Phe Ala	
1160 1165 1170	

aag cag ccg gcg tac acg ctg gta gac aga gaa gag aag ccc ccc aac 3969
 Lys Gln Pro Ala Tyr Thr Leu Val Asp Arg Glu Glu Lys Pro Pro Asn
 1175 1180 1185

ggc acg ccg aca aaa cac cca aac tgg aca aac aaa cag gac aac aga 4017
 Gly Thr Pro Thr Lys His Pro Asn Trp Thr Asn Lys Gln Asp Asn Arg
 1190 1195 1200

gac ttg gaa agt gcc cag agc tta aac cga atg gag tac atc gta 4062
 Asp Leu Glu Ser Ala Gln Ser Leu Asn Arg Met Glu Tyr Ile Val
 1205 1210 1215

tagcagaccg cgggcactgc cgccgctagg tagagtctga gggctttag ttccttaaac 4122

tgtcgtgtca tactcgagtc tgaggccggt gctgacttag aatccctgtg ttaatttaag 4182

ttttgacaag ctggcattaca ctggca 4208

<210> 11
 <211> 1218
 <212> PRT
 <213> Homo sapiens

<400> 11
 Met Arg Ser Pro Arg Thr Arg Gly Arg Ser Gly Arg Pro Leu Ser Leu
 1 5 10 15

Leu Leu Ala Leu Leu Cys Ala Leu Arg Ala Lys Val Cys Gly Ala Ser
 20 25 30

Gly Gln Phe Glu Leu Glu Ile Leu Ser Met Gln Asn Val Asn Gly Glu
 35 40 45

Leu Gln Asn Gly Asn Cys Cys Gly Gly Ala Arg Asn Pro Gly Asp Arg
 50 55 60

Lys Cys Thr Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu Lys
 65 70 75 80

Glu Tyr Gln Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly Ser
 85 90 95

Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala Ser
 100 105 110

Arg Gly Asn Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala Trp
 115 120 125

Pro Arg Ser Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn Asp
 130 135 140

Thr Val Gln Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly Met
 145 150 155 160

Ile Asn Pro Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly Val
 165 170 175

0099553 112904
 T06211 112904

Ala His Phe Glu Tyr Gln Ile Arg Val Thr Cys Asp Asp Tyr Tyr Tyr
 180 185 190
 Gly Phe Gly Cys Asn Lys Phe Cys Arg Pro Arg Asp Asp Phe Phe Gly
 195 200 205
 His Tyr Ala Cys Asp Gln Asn Gly Asn Lys Thr Cys Met Glu Gly Trp
 210 215 220
 Met Gly Pro Glu Cys Asn Arg Ala Ile Cys Arg Gln Gly Cys Ser Pro
 225 230 235 240
 Lys His Gly Ser Cys Lys Leu Pro Gly Asp Cys Arg Cys Gln Tyr Gly
 245 250 255
 Trp Gln Gly Leu Tyr Cys Asp Lys Cys Ile Pro His Pro Gly Cys Val
 260 265 270
 His Gly Ile Cys Asn Glu Pro Trp Gln Cys Leu Cys Glu Thr Asn Trp
 275 280 285
 Gly Gly Gln Leu Cys Asp Lys Asp Leu Asn Tyr Cys Gly Thr His Gln
 290 295 300
 Pro Cys Leu Asn Gly Gly Thr Cys Ser Asn Thr Gly Pro Asp Lys Tyr
 305 310 315 320
 Gln Cys Ser Cys Pro Glu Gly Tyr Ser Gly Pro Asn Cys Glu Ile Ala
 325 330 335
 Glu His Ala Cys Leu Ser Asp Pro Cys His Asn Arg Gly Ser Cys Lys
 340 345 350
 Glu Thr Ser Leu Gly Phe Glu Cys Glu Cys Ser Pro Gly Trp Thr Gly
 355 360 365
 Pro Thr Cys Ser Thr Asn Ile Asp Asp Cys Ser Pro Asn Asn Cys Ser
 370 375 380
 His Gly Gly Thr Cys Gln Asp Leu Val Asn Gly Phe Lys Cys Val Cys
 385 390 395 400
 Pro Pro Gln Trp Thr Gly Lys Thr Cys Gln Leu Asp Ala Asn Glu Cys
 405 410 415
 Glu Ala Lys Pro Cys Val Asn Ala Lys Ser Cys Lys Asn Leu Ile Ala
 420 425 430
 Ser Tyr Tyr Cys Asp Cys Leu Pro Gly Trp Met Gly Gln Asn Cys Asp
 435 440 445
 Ile Asn Ile Asn Asp Cys Leu Gly Gln Cys Gln Asn Asp Ala Ser Cys
 450 455 460
 Arg Asp Leu Val Asn Gly Tyr Arg Cys Ile Cys Pro Pro Gly Tyr Ala
 465 470 475 480

0095593-12901

Gly Asp His Cys Glu Arg Asp Ile Asp Glu Cys Ala Ser Asn Pro Cys
 485 490 495
 Leu Asn Gly Gly His Cys Gln Asn Glu Ile Asn Arg Phe Gln Cys Leu
 500 505 510
 Cys Pro Thr Gly Phe Ser Gly Asn Leu Cys Gln Leu Asp Ile Asp Tyr
 515 520 525
 Cys Glu Pro Asn Pro Cys Gln Asn Gly Ala Gln Cys Tyr Asn Arg Ala
 530 535 540
 Ser Asp Tyr Phe Cys Lys Cys Pro Glu Asp Tyr Glu Gly Lys Asn Cys
 545 550 555 560
 Ser His Leu Lys Asp His Cys Arg Thr Thr Pro Cys Glu Val Ile Asp
 565 570 575
 Ser Cys Thr Val Ala Met Ala Ser Asn Asp Thr Pro Glu Gly Val Arg
 580 585 590
 Tyr Ile Ser Ser Asn Val Cys Gly Pro His Gly Lys Cys Lys Ser Gln
 595 600 605
 Ser Gly Gly Lys Phe Thr Cys Asp Cys Asn Lys Gly Phe Thr Gly Thr
 610 615 620
 Tyr Cys His Glu Asn Ile Asn Asp Cys Glu Ser Asn Pro Cys Arg Asn
 625 630 635 640
 Gly Gly Thr Cys Ile Asp Gly Val Asn Ser Tyr Lys Cys Ile Cys Ser
 645 650 655
 Asp Gly Trp Glu Gly Ala Tyr Cys Glu Thr Asn Ile Asn Asp Cys Ser
 660 665 670
 Gln Asn Pro Cys His Asn Gly Gly Thr Cys Arg Asp Leu Val Asn Asp
 675 680 685
 Phe Tyr Cys Asp Cys Lys Asn Gly Trp Lys Gly Lys Thr Cys His Ser
 690 695 700
 Arg Asp Ser Gln Cys Asp Glu Ala Thr Cys Asn Asn Gly Gly Thr Cys
 705 710 715 720
 Tyr Asp Glu Gly Asp Ala Phe Lys Cys Met Cys Pro Gly Gly Trp Glu
 725 730 735
 Gly Thr Thr Cys Asn Ile Ala Arg Asn Ser Ser Cys Leu Pro Asn Pro
 740 745 750
 Cys His Asn Gly Gly Thr Cys Val Val Asn Gly Glu Ser Phe Thr Cys
 755 760 765
 Val Cys Lys Glu Gly Trp Glu Gly Pro Ile Cys Ala Gln Asn Thr Asn
 770 775 780

FOOET E65660

Asp Cys Ser Pro His Pro Cys Tyr Asn Ser Gly Thr Cys Val Asp Gly
 785 790 795 800
 Asp Asn Trp Tyr Arg Cys Glu Cys Ala Pro Gly Phe Ala Gly Pro Asp
 805 810 815
 Cys Arg Ile Asn Ile Asn Glu Cys Gln Ser Ser Pro Cys Ala Phe Gly
 820 825 830
 Ala Thr Cys Val Asp Glu Ile Asn Gly Tyr Arg Cys Val Cys Pro Pro
 835 840 845
 Gly His Ser Gly Ala Lys Cys Gln Glu Val Ser Gly Arg Pro Cys Ile
 850 855 860
 Thr Met Gly Ser Val Ile Pro Asp Gly Ala Lys Trp Asp Asp Asp Cys
 865 870 875 880
 Asn Thr Cys Gln Cys Leu Asn Gly Arg Ile Ala Cys Ser Lys Val Trp
 885 890 895
 Cys Gly Pro Arg Pro Cys Leu Leu His Lys Gly His Ser Glu Cys Pro
 900 905 910
 Ser Gly Gln Ser Cys Ile Pro Ile Leu Asp Asp Gln Cys Phe Val His
 915 920 925
 Pro Cys Thr Gly Val Gly Glu Cys Arg Ser Ser Ser Leu Gln Pro Val
 930 935 940
 Lys Thr Lys Cys Thr Ser Asp Ser Tyr Tyr Gln Asp Asn Cys Ala Asn
 945 950 955 960
 Ile Thr Phe Thr Phe Asn Lys Glu Met Met Ser Pro Gly Leu Thr Thr
 965 970 975
 Glu His Ile Cys Ser Glu Leu Arg Asn Leu Asn Ile Leu Lys Asn Val
 980 985 990
 Ser Ala Glu Tyr Ser Ile Tyr Ile Ala Cys Glu Pro Ser Pro Ser Ala
 995 1000 1005
 Asn Asn Glu Ile His Val Ala Ile Ser Ala Glu Asp Ile Arg Asp Asp
 1010 1015 1020
 Gly Asn Pro Ile Lys Glu Ile Thr Asp Lys Ile Ile Asp Leu Val Ser
 1025 1030 1035 1040
 Lys Arg Asp Gly Asn Ser Ser Leu Ile Ala Ala Val Ala Glu Val Arg
 1045 1050 1055
 Val Gln Arg Arg Pro Leu Lys Asn Arg Thr Asp Phe Leu Val Pro Leu
 1060 1065 1070
 Leu Ser Ser Val Leu Thr Val Ala Trp Ile Cys Cys Leu Val Thr Ala
 1075 1080 1085

009559-12901
 10621-1655560


```
<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence
```

```
<400> 14
tgqcartgya aytgycarga                20
```

```
<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

```
<400> 15
atyttytyt crcarttraa 20
```

```
<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

```
<220>  
<221> modified_base  
<222> (12)  
<223> a, t, c, g, other or unknown
```

```
<400> 16
tgcststgyg anaccaactg                20
```

```
<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

20

<220>
<223> Description of Artificial Sequence: Chemical
Synthesis

25

```
<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

25

```
<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

28

```
<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

28

```
<210> 22
<211> 55
```

<212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
 Synthesis

<400> 22

tcatttatca tcatcatctt tataatcccc gccctggccc tctagcttct cagtg 55

<210> 23

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
 Synthesis

<400> 23

aaccatcccc gaggggtgtct gctggaagcc aggctca 37

<210> 24

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
 Synthesis

<400> 24

cctctagagt cgcggccgtc gcaactcattt acc 33

<210> 25

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
 Synthesis

<400> 25

aaggatcccc gccctggccc tctagcttc 29

<210> 26

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
 Synthesis

0996593 11901

36

```
<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

25

```
<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

28

```
<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

51

```
<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

25

<210> 31
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
 Synthesis

<400> 31
 ggaattcgat atcaagctta tcgat

25

<210> 32
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
 Synthesis

<400> 32
 tcaatctggt ctggtgttca gaggccg

27

<210> 33
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
 Synthesis

<400> 33
 ggacgcgtgg atccactagt tctagagc

28

<210> 34
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
 Synthesis

<400> 34
 tcatttatca tcatcatctt tataatcatc tggtctgttg ttcagaggcc g

51

<210> 35
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>

005211 E655550

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 35

aaggatccgt tctgttggtc agaggccgcc t

31

<210> 36

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 36

cctctagacg cgtagagcgg ccgccaccgc ggtgga

36

<210> 37

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 37

ctatacgatg tactccattc ggtttaag

28

<210> 38

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 38

ggacgcgtct agagtcgacc tgcaggcatg c

31

<210> 39

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 39

ctatttatca tcatcatctt tataatctac gatgtactcc attcggttta ag

52

0095591290
T0621 E555550

<210> 40
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus

<220>
 <221> MOD_RES
 <222> (1)..(45)
 <223> "Xaa" represents a variable amino acid

<400> 40
 Xaa Xaa Cys Xaa Xaa Xaa Tyr Tyr Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Xaa Phe Gly His Xaa Xaa Cys Xaa Xaa Xaa Gly
 20 25 30
 Xaa Xaa Xaa Cys Xaa Xaa Gly Trp Xaa Gly Xaa Xaa Cys
 35 40 45

<210> 41
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 41
 Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly
 20 25 30
 Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys
 35 40 45

<210> 42
 <211> 45
 <212> PRT
 <213> Drosophila sp.

<400> 42
 Val Thr Cys Asp Leu Asn Tyr Tyr Gly Ser Gly Cys Ala Lys Phe Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Ser Phe Gly His Ser Thr Cys Ser Glu Thr Gly
 20 25 30
 Glu Ile Ile Cys Leu Thr Gly Trp Gln Gly Asp Tyr Cys
 35 40 45

<210> 43

0955591200
 T062T E655560

<211> 45
 <212> PRT
 <213> *Xenopus laevis*

<400> 43
 Phe Val Cys Asp Glu Tyr Tyr Tyr Gly Glu Gly Cys Ser Asp Tyr Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Ala Phe Gly His Phe Ser Cys Gly Glu Arg Gly
 20 25 30
 Glu Lys Leu Cys Asn Pro Gly Trp Lys Gly Leu Tyr Cys
 35 40 45

<210> 44
 <211> 45
 <212> PRT
 <213> *Gallus sp.*

<400> 44
 Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Arg Phe Gly His Phe Thr Cys Gly Glu Arg Gly
 20 25 30
 Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Gln Tyr Cys
 35 40 45

<210> 45
 <211> 45
 <212> PRT
 <213> *Murine sp.*

<400> 45
 Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Asp Arg Gly
 20 25 30
 Glu Lys Met Cys Asp Pro Gly Trp Lys Gly Gln Tyr Cys
 35 40 45

<210> 46
 <211> 45
 <212> PRT
 <213> *Homo sapiens*

<400> 46
 Val Thr Cys Asp Asp Tyr Tyr Tyr Gly Phe Gly Cys Asn Lys Phe Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Phe Phe Gly His Tyr Ala Cys Asp Gln Asn Gly
 20 25 30

009559 E655550


```

<400> 48
Val Thr Cys Asp Asp His Tyr Tyr Gly Phe Gly Cys Asn Lys Phe Cys
  1                    5                10                15
Arg Pro Arg Asp Asp Phe Phe Gly His Tyr Ala Cys Asp Gln Asn Gly
          20                25                30
Asn Lys Thr Cys Met Glu Gly Trp Met Gly Pro Glu Cys
      35                40                45

```